#3

OIPE

RAW SEQUENCE LISTING   DATE: 02/14/2002
PATENT APPLICATION: US/10/054,579   TIME: 16:11:10

Input Set : A:\LEX-0300-USA SEQLIST.txt
Output Set: N:\CRF3\02142002\J054579.raw

ENTERED

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      4 <110> APPLICANT: Turner, C. Alexander Jr.
      5        Mathur, Brian
      7 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
      9 <130> FILE REFERENCE: LEX-0300-USA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/054,579
C--> 11 <141> CURRENT FILING DATE: 2002-01-22
     11 <150> PRIOR APPLICATION NUMBER: US 60/263,378
     12 <151> PRIOR FILING DATE: 2001-01-23
     14 <160> NUMBER OF SEQ ID NOS: 4
     16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     18 <210> SEQ ID NO: 1
     19 <211> LENGTH: 2007
     20 <212> TYPE: DNA
     21 <213> ORGANISM: homo sapiens
     23 <400> SEQUENCE: 1
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     25 ctggagaaga cgctgggcaa ggggcagaca ggtctggtga agctgggggt tcactgcgtc 120
     26 acctgccaga aggtggccat caagatcgtc aaccgtgaga agctcagcga gtcggtgctg 180
     27 atgaaggtgg agcgggagat cgcgatcctg aagctcattg agcaccccca cgtcctaaag 240
     28 ctgcacgacg tttatgaaaa caaaaaatat ttgtacctgg tgctagaaca cgtgtcaggt 300
     29 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaagga ggctcggaag 360
     30 ttcttccggc agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 420
     31 gatctgaaac ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 480
     32 ggcatggcgt ccctgcaggt tggcgacagc ctgttggaga ccagctgtgg gtccccccac 540
     33 tacgcctgcc ccgaggtgat ccggggggag aagtatgacg gccggaaggc ggacgtgtgg 600
     34 agctgcggcg tcatcctgtt cgccttgctg gtgggggctc tgcccttcga cgatgacaac 660
     35 ttgcgacagc tgctggagaa ggtgaagcgg ggcgtgttcc acatgccgca ctttatcccg 720
     36 cccgactgcc agagtctgct acggggcatg atcgaggtgg acgccgcacg ccgcctcacg 780
     37 ctagagcaca ttcagaaaca catatggtat atagggggca agaatgagcc cgaaccagag 840
     38 cagcccattc ctcgcaaggt gcagatccgc tcgctgccca gcctggagga catcgacccc 900
     39 gacgtgctgg acagcatgca ctcactgggc tgcttccgag accgcaacaa gctgctgcag 960
     40 gacctgctgt ccgaggagga gaaccaggag aagatgattt acttcctcct cctggaccgg 1020
     41 aaagaaaggt acccgagcca ggaggatgag gacctgcccc cccggaacga gatagaccct 1080
     42 cccccggaagc gtgtggactc cccgatgctg aaccggcacg gcaagcggcg gccagaacgc 1140
     43 aaatccatgg aggtgctcag cgtgacggac ggcggctccc cggtgcctgc gcggcgggcc 1200
     44 attgagatgg cccagcacgg ccagaggtct cggtccatca gcggtgcctc ctcaggcctt 1260
     45 tccaccagcc cactcagcag cccccgggtg accccctcacc cctcaccaag gggcagtccc 1320
     46 ctccccaccc ccaaggggac acctgtccac acgccaaagg agagcccggc tggcacgccc 1380
     47 aaccccacgc ccccgtccag ccccagcgtc ggaggggtgc cctggagggc gcggctcaac 1440
     48 tccatcaaga acagctttct gggctcaccc cgcttccacc gccggaaact gcaagttccg 1500
     49 acgccggagg agatgtccaa cctgacacca gagtcgtccc cagagctggc gaagaagtcc 1560
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Input Set : A:\LEX-0300-USA SEQLIST.txt
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52 agccacagcg tcatctccca aacgagcttc cgggccgagt acaaggccac gggggggcca 1740
53 gccgtgttcc agaagccggt caagttccag gttgatatca cctacacgga gggtggggag 1800
54 gcgcagaagg agaacggcat ctactccgtc accttcaccc tgctctcagg ccccagccgt 1860
55 cgcttcaaga gggtggtgga gaccatccag gcccagctgc tgagcacaca cgacccgcct 1920
56 gcggcccagc acttgtcaga caccactaac tgtatggaaa tgatgacggg gcggctttcc 1980
57 aaatgtggaa ttatcccgaa aagttaa                                    2007
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 668
61 <212> TYPE: PRT
62 <213> ORGANISM: homo sapiens
64 <400> SEQUENCE: 2
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66  1               5                   10                  15
67 Gly Pro Tyr Arg Leu Glu Lys Thr Leu Gly Lys Gly Gln Thr Gly Leu
68              20                  25                  30
69 Val Lys Leu Gly Val His Cys Val Thr Cys Gln Lys Val Ala Ile Lys
70          35                  40                  45
71 Ile Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu
72      50                  55                  60
73 Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys
74 65                  70                  75                  80
75 Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu
76              85                  90                  95
77 His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg
78              100                 105                 110
79 Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Ile Ser Ala
80          115                 120                 125
81 Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg Asp Leu Lys Pro
82      130                 135                 140
83 Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe
84 145                 150                 155                 160
85 Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys
86              165                 170                 175
87 Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg Gly Glu Lys Tyr
88              180                 185                 190
89 Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val Ile Leu Phe Ala
90          195                 200                 205
91 Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu
92      210                 215                 220
93 Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro
94 225                 230                 235                 240
95 Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Asp Ala Ala
96              245                 250                 255
97 Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile Trp Tyr Ile Gly
98              260                 265                 270
99 Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro Arg Lys Val Gln
100          275                 280                 285
101 Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro Asp Val Leu Asp
102      290                 295                 300
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RAW SEQUENCE LISTING   DATE: 02/14/2002
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Input Set : **A:\LEX-0300-USA SEQLIST.txt**
Output Set: **N:\CRF3\02142002\J054579.raw**

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103 Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn Lys Leu Leu Gln
104 305                 310             315                 320
105 Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Phe Leu
106             325             330                 335
107 Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu Asp Glu Asp Leu
108             340             345                 350
109 Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg Val Asp Ser Pro
110         355             360                 365
111 Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met Glu
112     370                 375                 380
113 Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro Ala Arg Arg Ala
114 385                 390                 395                 400
115 Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser Ile Ser Gly Ala
116             405                 410                 415
117 Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro Arg Val Thr Pro
118             420                 425                 430
119 His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro Lys Gly Thr Pro
120         435             440                 445
121 Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro Asn Pro Thr Pro
122     450                 455                 460
123 Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg Ala Arg Leu Asn
124 465                 470                 475                 480
125 Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe His Arg Arg Lys
126             485                 490                 495
127 Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu Thr Pro Glu Ser
128             500                 505                 510
129 Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn Phe Ile Ser Leu
130         515                 520                 525
131 Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp Lys Pro Leu Ser
132     530                 535                 540
133 Ser Ile Lys Ala Asp Ile Val His Ala Phe Leu Ser Ile Pro Ser Leu
134 545                 550                 555                 560
135 Ser His Ser Val Ile Ser Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala
136             565                 570                 575
137 Thr Gly Gly Pro Ala Val Phe Gln Lys Pro Val Lys Phe Gln Val Asp
138             580                 585                 590
139 Ile Thr Tyr Thr Glu Gly Gly Glu Ala Gln Lys Glu Asn Gly Ile Tyr
140         595                 600                 605
141 Ser Val Thr Phe Thr Leu Leu Ser Gly Pro Ser Arg Arg Phe Lys Arg
142     610                 615                 620
143 Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Pro Pro
144 625                 630                 635                 640
145 Ala Ala Gln His Leu Ser Asp Thr Thr Asn Cys Met Glu Met Met Thr
146             645                 650                 655
147 Gly Arg Leu Ser Lys Cys Gly Ile Ile Pro Lys Ser
148             660                 665
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 1827
153 <212> TYPE: DNA
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154 <213> ORGANISM: homo sapiens
156 <400> SEQUENCE: 3
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158 ctgcacgacg tttatgaaaa caaaaaatat ttgtacctgg tgctagaaca cgtgtcaggt 120
159 ggtgagctct tcgactacct ggtgaagaag gggaggctga cgcctaagga ggctcggaag 180
160 ttcttccggc agatcatctc tgcgctggac ttctgccaca gccactccat atgccacagg 240
161 gatctgaaac ctgaaaacct cctgctggac gagaagaaca acatccgcat cgcagacttt 300
162 ggcatggcgt ccctgcaggt tggcgacagc ctgttggaga ccagctgtgg gtccccccac 360
163 tacgcctgcc ccgaggtgat ccggggggag aagtatgacg gccggaaggc ggacgtgtgg 420
164 agctgcggcg tcatcctgtt cgccttgctg gtggggggctc tgcccttcga cgatgacaac 480
165 ttgcgacagc tgctggagaa ggtgaagcgg ggcgtgttcc acatgccgca ctttatcccg 540
166 cccgactgcc agagtctgct acggggcatg atcgaggtgg acgccgcacg ccgcctcacg 600
167 ctagagcaca ttcagaaaca catatggtat ataggggca  agaatgagcc cgaaccagag 660
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169 gacgtgctgg acagcatgca ctcactgggc tgcttccgag accgcaacaa gctgctgcag 780
170 gacctgctgt ccgaggagga gaaccaggag aagatgattt acttcctcct cctggaccgg 840
171 aaagaaaggt acccgagcca ggaggatgag gacctgcccc cccggaacga gatagaccct 900
172 ccccggaagc gtgtggactc cccgatgctg aaccggcacg gcaagcggcg gccagaacgc 960
173 aaatccatgg aggtgctcag cgtgacggac ggcggctccc cggtgcctgc gcggcgggcc 1020
174 attgagatgg cccagcacgg ccagaggtct cggtccatca gcggtgcctc ctcaggcctt 1080
175 tccaccagcc cactcagcag ccccggggtg accctcacc cctcaccaag gggcagtccc 1140
176 ctccccaccc ccaaggggac acctgtccac acgccaaagg agagcccggc tggcacgccc 1200
177 aaccccacgc ccccgtccag ccccagcgtc ggaggggtgc cctggagggc gcggctcaac 1260
178 tccatcaaga acagctttct gggctcaccc cgcttccacc gccggaaact gcaagttccg 1320
179 acgccggagg agatgtccaa cctgacacca gagtcgtccc cagagctggc gaagaagtcc 1380
180 tggtttggga acttcatcag cctggagaag gaggagcaga tcttcgtggt catcaaagac 1440
181 aaacctctga gctccatcaa ggctgacatc gtgcacgcct tcctgtcgat tcccagtctc 1500
182 agccacagcg tcatctccca aacgagcttc cgggccgagt acaaggccac ggggggggcca 1560
183 gccgtgttcc agaagccggt caagttccag gttgatatca cctacacgga gggtgggggag 1620
184 gcgcagaagg agaacggcat ctactccgtc accttcaccc tgctctcagg ccccagccgt 1680
185 cgcttcaaga gggtggtgga gaccatccag gcccagctgc tgagcacaca cgacccgcct 1740
186 gcggcccagc acttgtcaga caccactaac tgtatggaaa tgatgacggg gcggctttcc 1800
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189 <210> SEQ ID NO: 4
190 <211> LENGTH: 608
191 <212> TYPE: PRT
192 <213> ORGANISM: homo sapiens
194 <400> SEQUENCE: 4
195 Met Lys Val Glu Arg Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro
196 1               5                   10                  15
197 His Val Leu Lys Leu His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr
198             20                  25                  30
199 Leu Val Leu Glu His Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val
200         35                  40                  45
201 Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln
202     50                  55                  60
203 Ile Ile Ser Ala Leu Asp Phe Cys His Ser His Ser Ile Cys His Arg
204 65                  70                  75                  80
205 Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg
```

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206                     85                    90                    95
207 Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu
208                     100                   105                   110
209 Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Arg
210             115                   120                   125
211 Gly Glu Lys Tyr Asp Gly Arg Lys Ala Asp Val Trp Ser Cys Gly Val
212         130                   135                   140
213 Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn
214 145                   150                   155                   160
215 Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro
216                 165                   170                   175
217 His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu
218                 180                   185                   190
219 Val Asp Ala Ala Arg Arg Leu Thr Leu Glu His Ile Gln Lys His Ile
220             195                   200                   205
221 Trp Tyr Ile Gly Gly Lys Asn Glu Pro Glu Pro Glu Gln Pro Ile Pro
222     210                   215                   220
223 Arg Lys Val Gln Ile Arg Ser Leu Pro Ser Leu Glu Asp Ile Asp Pro
224 225                   230                   235                   240
225 Asp Val Leu Asp Ser Met His Ser Leu Gly Cys Phe Arg Asp Arg Asn
226                 245                   250                   255
227 Lys Leu Leu Gln Asp Leu Leu Ser Glu Glu Glu Asn Gln Glu Lys Met
228                 260                   265                   270
229 Ile Tyr Phe Leu Leu Leu Asp Arg Lys Glu Arg Tyr Pro Ser Gln Glu
230             275                   280                   285
231 Asp Glu Asp Leu Pro Pro Arg Asn Glu Ile Asp Pro Pro Arg Lys Arg
232     290                   295                   300
233 Val Asp Ser Pro Met Leu Asn Arg His Gly Lys Arg Arg Pro Glu Arg
234 305                   310                   315                   320
235 Lys Ser Met Glu Val Leu Ser Val Thr Asp Gly Gly Ser Pro Val Pro
236                 325                   330                   335
237 Ala Arg Arg Ala Ile Glu Met Ala Gln His Gly Gln Arg Ser Arg Ser
238             340                   345                   350
239 Ile Ser Gly Ala Ser Ser Gly Leu Ser Thr Ser Pro Leu Ser Ser Pro
240         355                   360                   365
241 Arg Val Thr Pro His Pro Ser Pro Arg Gly Ser Pro Leu Pro Thr Pro
242     370                   375                   380
243 Lys Gly Thr Pro Val His Thr Pro Lys Glu Ser Pro Ala Gly Thr Pro
244 385                   390                   395                   400
245 Asn Pro Thr Pro Pro Ser Ser Pro Ser Val Gly Gly Val Pro Trp Arg
246                 405                   410                   415
247 Ala Arg Leu Asn Ser Ile Lys Asn Ser Phe Leu Gly Ser Pro Arg Phe
248             420                   425                   430
249 His Arg Arg Lys Leu Gln Val Pro Thr Pro Glu Glu Met Ser Asn Leu
250         435                   440                   445
251 Thr Pro Glu Ser Ser Pro Glu Leu Ala Lys Lys Ser Trp Phe Gly Asn
252     450                   455                   460
253 Phe Ile Ser Leu Glu Lys Glu Glu Gln Ile Phe Val Val Ile Lys Asp
254 465                   470                   475                   480
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VERIFICATION SUMMARY   DATE: 02/14/2002
PATENT APPLICATION: US/10/054,579   TIME: 16:11:11

Input Set : **A:\LEX-0300-USA SEQLIST.txt**
Output Set: **N:\CRF3\02142002\J054579.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date